



# SEQUENCE LISTING

<110> Freyssinet, Georges  
Rang, Cecile  
Frutos, Roger

<120> Pepsin-sensitive modified Bacillus thuringiensis insecticidal toxin

<130> A35992-PCT-USA-A (072667.0191)

<140> 10/665,460

<141> 2003-09-19

<150> PCT/FR02/00772

<151> 2002-03-04

<150> FR 01/03691

<151> 2001-03-19

<160> 160

<170> PatentIn Ver. 2.1

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<211> 2019

<212> DNA

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610 615 620	
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Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly		
625					630					635					640		
gtt	agc	acc	ggg	ggg	gaa	tat	tat	ata	gat	aga	att	gaa	att	gtc	cct	1968	
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro		
			645						650					655			
gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	gcg	gcg	aag	aaa	2016	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys		
			660					665					670				
gcg																2019	
Ala																	

<210> 4  
 <211> 673  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Artificial sequence description: Cry9Ca1 Leu-164

<400> 4

Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His		
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Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp		
			20					25					30				
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met		
		35					40					45					
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile		
		50				55					60						
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile		
65					70					75					80		
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr		
				85					90					95			
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp		
		100					105						110				
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr		
		115					120					125					
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp		
		130				135					140						
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg		
145					150					155					160		
Asn	Asp	Thr	Leu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu		
				165					170						175		

Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln		
			180					185					190				
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu		
		195					200					205					
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr		
	210					215					220						
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala		
225					230					235					240		
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg		
				245					250					255			
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg		
			260					265					270				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr		
	275						280					285					
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg		
	290					295					300						
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly		
305					310					315					320		
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu		
				325					330					335			
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
		340						345					350				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp		
	355						360					365					
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala		
	370					375					380						
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile		
385					390					395					400		
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp		
			405						410					415			
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
	435						440					445					
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
	450					455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr  
                     485                    490                    495  
 Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro  
                     500                    505                    510  
 Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser  
                     515                    520                    525  
 Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu  
                     530                    535                    540  
 Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
                     545                    550                    555                    560  
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr  
                     565                    570                    575  
 Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
                     580                    585                    590  
 Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
                     595                    600                    605  
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro  
                     610                    615                    620  
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
                     625                    630                    635                    640  
 Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
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 Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys  
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 Ala

<210> 5  
 <211> 2019  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Artificial sequence description: Cry9Ca1 Phe-164

<220>  
 <221> CDS  
 <222> (1) .. (2019)

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tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac	96
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	
cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	
aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att	192
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata	240
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile	
65 70 75 80	
ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca ttt aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Phe Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	

aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly	
305 310 315 320	
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc	1008
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu	
325 330 335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg aat agc	1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser	
340 345 350	
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat	1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp	
355 360 365	
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca	1152
Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala	
370 375 380	
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att	1200
Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile	
385 390 395 400	
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat	1248
Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp	
405 410 415	
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt	1296
Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe	
420 425 430	
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga	1344
Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly	
435 440 445	
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt	1392
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser	
450 455 460	
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt	1440

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe	
465 470 475 480	
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggg act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 6

<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Phe-164

<400> 6

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Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
65					70					75					80	
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
				85					90					95		
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
		100						105					110			
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
	115						120				125					
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155				160		
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
		180						185					190			
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
		195					200					205				
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230					235					240	
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	
			245						250					255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			



Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	275	280	285
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	290	295	300
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	305	310	315
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	325	330	335
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	340	345	350
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	355	360	365
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	370	375	380
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	385	390	395
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	405	410	415
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	420	425	430
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	435	440	445
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	450	455	460
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	465	470	475
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	485	490	495
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	500	505	510
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	515	520	525
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	530	535	540
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	545	550	555
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	565	570	575

Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
                   580                                  585                                  590  
 Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
                   595                                  600                                  605  
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro  
           610                                  615                                  620  
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
   625                                  630                                  635                                  640  
 Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
                   645                                  650                                  655  
 Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys  
                   660                                  665                                  670  
 Ala

<210> 7  
 <211> 2019  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Artificial sequence description: Cry9Ca1 Glu-164

<220>  
 <221> CDS  
 <222> (1)..(2019)

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 tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96  
 Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
                   20                                  25                                  30  
 cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144  
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
                   35                                  40                                  45  
 aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att 192  
 Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
           50                                  55                                  60  
 agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata 240  
 Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
   65                                  70                                  75                                  80

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca gaa aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960

Glu 305	Val	Tyr	Thr	Asp	Pro 310	Ile	Val	Phe	Asn	Pro 315	Pro	Ala	Asn	Val	Gly 320	
ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
		355					360					365				
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405					410					415		
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
465					470				475						480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
			485					490						495		
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
		515					520					525				
ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	

530	535	540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat			1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn			
545	550	555	560
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca			1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr			
	565	570	575
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat			1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp			
	580	585	590
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa			1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu			
	595	600	605
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct			1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro			
	610	615	620
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt			1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly			
625	630	635	640
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct			1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro			
	645	650	655
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa			2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys			
	660	665	670
gcg			2019
Ala			

<210> 8

<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Glu-164

<400> 8

Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His
1				5					10					15	

Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp
			20					25					30		

Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
	35						40					45			

Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile 65 70 75 80		
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr 85 90 95		
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp 100 105 110		
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr 115 120 125		
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp 130 135 140		
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg 145 150 155 160		
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu 165 170 175		
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln 180 185 190		
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu 195 200 205		
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr 210 215 220		
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala 225 230 235 240		
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg 245 250 255		
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg 260 265 270		
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr 275 280 285		
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg 290 295 300		
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly 305 310 315 320		
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu 325 330 335		
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser 340 345 350		
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp		

355					360					365						
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
370					375					380						
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
405					410					415						
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
420					425					430						
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
435					440					445						
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
450					455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
485					490					495						
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
500					505					510						
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
515					520					525						
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
530					535					540						
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	
545					550					555					560	
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	
565					570					575						
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	
580					585					590						
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
595					600					605						
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
610					615					620						
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
625					630					635					640	
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro	
645					650					655						
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys	

660

665

670

Ala

&lt;210&gt; 9

&lt;211&gt; 2019

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Artificial sequence description: Cry9Ca1-100%

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2019)

&lt;400&gt; 9

atg aat cga aat aat caa aat gaa tat gaa att att gaa gcc ccc cat	48
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Glu Ala Pro His	
1 5 10 15	
tgt ggg tgt cca tca gaa gaa gaa tta agg tat cct ttg gca agt gaa	96
Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu	
20 25 30	
cca aat gca gcg tta caa aat atg aac tat aaa gaa tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met	
35 40 45	
aca gaa gag gaa tac act gaa tct tat ata aat cct agt tta tct att	192
Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
agt ggt aga gaa gca tta cag act gcg ctt act gtt att agg aga ata	240
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile	
65 70 75 80	
ctc ggg gct tta ggt tta ccg ttt tct gga caa ata tta agt ttt tat	288
Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg ttt cca tta aat gaa aca gct ata ttt	336
Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe	
100 105 110	
gaa gct ttc atg cga cag tta gag gaa ctt tta aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu	
130 135 140	
tct ttt aat tta tat caa cgt tcc ctt caa aat ttt ttg gct gaa cga	480



Ser	Phe	Asn	Leu	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Leu	Ala	Glu	Arg	
145					150					155					160	
aat	gaa	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Glu	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gaa	ctt	gaa	ttt	tta	aat	gct	att	cca	ttg	ttt	gca	tta	aat	gga	cag	576
Glu	Leu	Glu	Phe	Leu	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Leu	Asn	Gly	Gln	
			180					185					190			
cag	tta	cca	tta	ctg	tca	tta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624
Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	
		195					200					205				
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	ttt	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr	
	210					215					220					
cag	ggg	gaa	att	tcc	aca	tat	tat	gaa	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230				235						240	
aag	tac	act	aat	tac	tgt	gaa	act	ttt	tat	aat	aca	ggg	tta	gaa	cgt	768
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	
			245					250					255			
tta	aga	gga	aca	aat	act	gaa	agt	ttt	tta	aga	tat	cat	caa	ttc	cgt	816
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265				270				
aga	gaa	atg	act	tta	tta	tta	tta	gaa	tta	tta	gcg	cta	ttt	cca	tat	864
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr	
		275					280					285				
tat	gaa	tta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
	290					295					300					
gag	tta	tat	aca	gaa	ccg	att	tta	ttt	aat	cca	cca	gct	aat	tta	gga	960
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	
305					310				315					320		
ctt	tgc	cga	cgt	ttt	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gaa	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	tta	tca	tct	aat	ttt	atg	gaa	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu	
		355					360					365				
tat	ttt	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gaa	tca	gca	1152
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	

370	375	380	
tta caa gaa gaa agt tat ggc cta att aca acc aca aga gca aca att Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile 385 390 395 400			1200
aat ccc gga tta gaa gga aca aac cgc ata gag tca acg gca tta gaa Asn Pro Gly Leu Glu Gly Thr Asn Arg Ile Glu Ser Thr Ala Leu Glu 405 410 415			1248
ttt cgt tct gca ttg ata ggt ata tat ggc tta aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Leu Asn Arg Ala Ser Phe 420 425 430			1296
tta cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Leu Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435 440 445			1344
tgt aga gaa ctc tat gaa aca aat gaa gaa tta cca cca gaa gaa agt Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser 450 455 460			1392
acc gga agt tca acc cat aga cta tct cat tta acc ttt ttt agc ttt Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe 465 470 475 480			1440
caa act aat cag gct gga tct ata gct aat gca gga agt tta cct act Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr 485 490 495			1488
tat tta ttt acc cgt cgt gaa tta gaa ctt aat aat acg att acc cca Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro 500 505 510			1536
aat aga att aca caa tta cca ttg tta aag gca tct gca cct tta tcg Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser 515 520 525			1584
ggg act acg tta tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu 530 535 540			1632
cga aga aca act aat ggc aca ttt gga acg tta aga tta acg tta aat Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn 545 550 555 560			1680
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr 565 570 575			1728
gga aat ttc agt ata agg tta ctc cgt gga ggg tta tct atc ggt gaa Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu 580 585 590			1776
tta aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu 595 600 605			1824

tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca tta aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly	
625 630 635 640	
tta agc acc ggt ggt gaa tat tat ata gaa aga att gaa att tta cct	1968
Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro	
645 650 655	
tta aat ccg gca cga gaa gcg gaa gag gaa tta gaa gcg gcg aag aaa	2016
Leu Asn Pro Ala Arg Glu Ala Glu Glu Glu Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 10  
 <211> 673  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Artificial sequence description: Cry9Ca1-100%

<400> 10	
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Glu Ala Pro His	
1 5 10 15	
Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu	
20 25 30	
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met	
35 40 45	
Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile	
65 70 75 80	
Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr	
85 90 95	
Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe	
100 105 110	
Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr	
115 120 125	
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu	
130 135 140	

Ser	Phe	Asn	Leu	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Leu	Ala	Glu	Arg	145	150	155	160
Asn	Glu	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	165	170	175	
Glu	Leu	Glu	Phe	Leu	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Leu	Asn	Gly	Gln	180	185	190	
Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	195	200	205	
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr	210	215	220	
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	225	230	235	240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	245	250	255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	260	265	270	
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr	275	280	285	
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	290	295	300	
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	305	310	315	320
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	325	330	335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	340	345	350	
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu	355	360	365	
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	370	375	380	
Leu	Gln	Glu	Glu	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	385	390	395	400
Asn	Pro	Gly	Leu	Glu	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Leu	Glu	405	410	415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Leu	Asn	Arg	Ala	Ser	Phe	420	425	430	
Leu	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	435	440	445	

Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser  
 450 455 460  
 Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe  
 465 470 475 480  
 Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr  
 485 490 495  
 Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro  
 500 505 510  
 Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser  
 515 520 525  
 Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu  
 530 535 540  
 Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn  
 545 550 555 560  
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr  
 565 570 575  
 Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu  
 580 585 590  
 Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
 595 600 605  
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro  
 610 615 620  
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly  
 625 630 635 640  
 Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro  
 645 650 655  
 Leu Asn Pro Ala Arg Glu Ala Glu Glu Glu Leu Glu Ala Ala Lys Lys  
 660 665 670

Ala

<210> 11

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1-25%

<220>

<221> CDS

<222> (1)..(2019)

<400> 11

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Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His	
1 5 10 15	
tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac	96
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp	
20 25 30	
cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met	
35 40 45	
aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att	192
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
agt ggt aga gaa gca tta cag act gcg ctt acg tta tta ggg aga ata	240
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Leu Leu Gly Arg Ile	
65 70 75 80	
ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata tta agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca cga aat tta agt tta tta cgt gct caa ttt ata gct tta	528
Asn Asp Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct tta aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Leu Asn Leu His Leu	
195 200 205	
tta tta tta aaa gaa gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	

210	215	220	
cag ggg gaa att tcc aca tat tat gaa cgt caa ttg gaa cta acc gct Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala 225 230 235 240			720
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gaa cgt Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Glu Arg 245 250 255			768
tta aga gga aca aat act gaa agt ttt tta aga tat cat caa ttc cgt Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg 260 265 270			816
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr 275 280 285			864
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg 290 295 300			912
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat tta gga Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Leu Gly 305 310 315 320			960
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu 325 330 335			1008
gaa aat gcc ttc att cgc cca cca cat ctt ttt gaa agg ctg aat agc Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser 340 345 350			1056
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gaa Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Glu 355 360 365			1104
tat ttt tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala 370 375 380			1152
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile 385 390 395 400			1200
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp 405 410 415			1248
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe 420 425 430			1296
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435 440 445			1344

tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt	1392
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser	
450 455 460	
acc gga agt tca acc cat aga cta tct cat tta acc ttt ttt agc ttt	1440
Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe	
465 470 475 480	
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggg act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	



gcg  
Ala

2019

<210> 12  
<211> 673  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Ca1-25%

<400> 12

Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15

Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30

Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Leu Leu Gly Arg Ile  
65 70 75 80

Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr  
85 90 95

Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110

Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu  
130 135 140

Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160

Asn Asp Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu  
165 170 175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180 185 190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Leu Asn Leu His Leu  
195 200 205

Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr  
210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala  
225 230 235 240

Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg		
			245						250					255			
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg		
			260					265					270				
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr		
		275					280					285					
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg		
	290					295					300						
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly		
305					310					315					320		
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu		
				325					330					335			
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser		
			340					345					350				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Glu		
		355					360					365					
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala		
	370					375					380						
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile		
385					390					395					400		
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp		
				405					410					415			
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
		435					440					445					
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
	450					455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr		
				485					490					495			
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro		
			500					505					510				
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser		
		515					520					525					
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu		
	530					535					540						

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
 545 550 555 560  
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr  
 565 570 575  
 Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
 580 585 590  
 Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
 595 600 605  
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro  
 610 615 620  
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
 625 630 635 640  
 Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
 645 650 655  
 Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys  
 660 665 670

Ala

<210> 13  
 <211> 30  
 <212> DNA  
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<220>  
 <223> Artificial sequence description: mutant 1

<400> 13  
 gaattaaatg aattttttaa tttaagtgtt 30

<210> 14  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Artificial sequence description: mutant 2

<400> 14  
 gaattaaatg aattatttaa tttaagtgtt 30

<210> 15  
 <211> 30  
 <212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 3

<400> 15

gaattattag aattttttatt attaagtggt

30

<210> 16

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 4

<400> 16

gaattattag aattattatt attaagtggt

30

<210> 17

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 5

<400> 17

gaattattag aagaattatt attaagtggt

30

<210> 18

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 6

<400> 18

gaacgattag aattttttatt attaagtggt

30

<210> 19

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 7

<400> 19

gaacgattag aattattatt attaagtggt

30

<210> 20  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description: mutant 8  
  
 <400> 20  
 gaattagaag aattattatt attaagtggt 30  
  
 <210> 21  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description: mutant 9  
  
 <400> 21  
 gaattattag aagaagaaga attaagtggt 30  
  
 <210> 22  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description: mutant 10  
  
 <400> 22  
 tttttattaa atttattttt tttaccatta ctg 33  
  
 <210> 23  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description: mutant11  
  
 <400> 23  
 tttttattaa atttagaaga attaccatta ctg 33  
  
 <210> 24  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description: mutant 12  
  
 <400> 24

tttgaagaaa atttagaaga attaccatta ctg 33

<210> 25

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 13

<400> 25

tttgaagaaa atttttttatt atttccatta ctg 33

<210> 26

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 14

<400> 26

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<210> 27

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 15

<400> 27

tttttattaa attttgaaga atttccatta ctg 33

<210> 28

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 16

<400> 28

tttttattaa atgaattttt tgaaccatta ctg 33

<210> 29

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 17

<400> 29

cttttttag aattattttt attc

24

<210> 30

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 18

<400> 30

cttttttat tattattttt attc

24

<210> 31

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 19

<400> 31

cttttttag aagaatttga atta

24

<210> 32

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 20

<400> 32

ctttttgaag aagaatttga atta

24

<210> 33

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 21

<400> 33

ctttttgaag aattatttga agaa

24

<210> 34

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 22

<400> 34

ttattagaat taaat

15

<210> 35

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 23

<400> 35

ttattatnttt taaat

15

<210> 36

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 24

<400> 36

ttagaattat taaat

15

<210> 37

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 25

<400> 37

ttattatnttt ttaat

15

<210> 38

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: mutant 26

<400> 38

ttagaagaat taaat

15



<210> 39  
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 <223> Artificial sequence description: mutant 27  
  
 <400> 39  
 ttagaatttt taaat 15  
  
 <210> 40  
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 <223> Artificial sequence description: mutant 28  
  
 <400> 40  
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 <210> 41  
 <211> 15  
 <212> DNA  
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 <223> Artificial sequence description: mutant 29  
  
 <400> 41  
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 <210> 42  
 <211> 33  
 <212> DNA  
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 <220>  
 <223> Artificial sequence description:  
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 <400> 42  
 gatcgaaatg atacattaaa ttaagtgtt gtt 33  
  
 <210> 43  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Artificial sequence description:  
         oligonucleotide 2

<400> 43  
gatcgaaatg atacatttaa tttaagtgtt gtt 33

<210> 44  
<211> 33  
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<210> 45  
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cgaaatgata cagattatt aagtgttggtt cgt 33

<210> 46  
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oligonucleotide 5

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cgaaatgata cagagaatt aagtgttggtt cgt 33

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caaaattggt tggctgaatt attagaatta ttattatta 39

<210> 57

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caaaattggt tggctgaatt attagaagaa ttattatta 39

<210> 58

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caaaattggt tggctgaacg attagaattt ttattatta 39

<210> 59

<211> 39

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<400> 59

caaaattggt tggctgaacg attagaatta ttattatta 39

<210> 60

<211> 39

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caaaattggt tggctgaatt agaagaatta ttattatta 39

<210> 61

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caaaattggt tggctgaatt attagaagaa gaagaatta 39

<210> 62  
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<210> 63  
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<210> 64  
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<210> 65  
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<400> 65  
ttattaaatg gacagcagtt tccattactg tcagta 36

<210> 66  
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<400> 66  
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<210> 67  
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oligonucleotide 26

<400> 67  
gaagaaaatg gacagcagtt accattactg tcagta 36

<210> 68  
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oligonucleotide 27

<400> 68  
gaagaaaatg gacagcagtt tccattactg tcagta 36

<210> 69  
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oligonucleotide 28

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oligonucleotide 29

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ccattgtttt tattaaattt agaagaatta ccattactgt cagta 45

<210> 71  
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oligonucleotide 30

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oligonucleotide 31

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ccattgtttg aagaaaattt tttattattt ccattactgt cagta 45

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oligonucleotide 32

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<210> 74  
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<220>

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<400> 74

ccattgtttt tattaaattt tgaagaattt ccattactgt cagta

45

<210> 75

<211> 45

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<400> 75

ccattgtttt tattaaatga attttttgaa ccattactgt cagta

45

<210> 76

<211> 33

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<220>

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<400> 76

gatgcatctc tttttttaga aggatgggga ttc

33

<210> 77

<211> 36

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<220>

<223> Artificial sequence description:  
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gatgcatctc tttttttatt aggatgggga ttcaca

36

<210> 78

<211> 33

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<220>

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<400> 78  
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<210> 79  
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<220>  
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oligonucleotide 38

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ttagaaggat ggggattaac acagggggaa att 33

<210> 80  
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oligonucleotide 39

<400> 80  
gaagaaggat ggggagaaac acagggggaa att 33

<210> 81  
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oligonucleotide 40

<400> 81  
gcatctcttt ttttagaatt atttttattc acacaggggg aaatt 45

<210> 82  
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oligonucleotide 41

<400> 82  
gcatctcttt ttttattatt atttttattc acacaggggg aaatt 45

<210> 83

<211> 45  
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 gcacatctcttt ttttagaatt atttttattc acacaggggg aaatt 45  
  
 <210> 84  
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     oligonucleotide 43  
  
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 gcacatctcttt ttgaagaatt atttttattc acacaggggg aaatt 45  
  
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 <223> Artificial sequence description:  
     oligonucleotide 44  
  
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 gcacatctcttt ttgaagaatt attttttagaa acacaggggg aaatt 45  
  
 <210> 86  
 <211> 39  
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     oligonucleotide 45  
  
 <400> 86  
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 <211> 39  
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<223> Artificial sequence description:  
oligonucleotide 46

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ggtttagatc gtttattatt tttaaatact gaaagttgg

39

<210> 88  
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oligonucleotide 47

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ggtttagatc gtttagaatt attaaatact gaaagttgg

39

<210> 89  
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oligonucleotide 48

<400> 89  
ggtttagatc gtttattatt ttttaatact gaaagttgg

39

<210> 90  
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oligonucleotide 49

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39

<210> 91  
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39

<210> 92  
<211> 39  
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oligonucleotide 51

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<210> 93  
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oligonucleotide 52

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ggtttagatc gtttagaaga agaaaatact gaaagttgg 39

<210> 94  
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oligonucleotide 53

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tgaatatgaa attattgaag cccccattg 30

<210> 95  
<211> 40  
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oligonucleotide 54

<400> 95  
tgggtgtcca tcagaagaag aattaaggta tcctttggca 40

<210> 96  
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oligonucleotide 55

<400> 96

tcctttggca agtgaaccaa atgcagc

27

<210> 97

<211> 25

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<223> Artificial sequence description:  
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gaactataaa gaatacttac aaatg

25

<210> 98

<211> 26

<212> DNA

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<223> Artificial sequence description:  
oligonucleotide 57

<400> 98

caaatgacag aagaggaata cactga

26

<210> 99

<211> 20

<212> DNA

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oligonucleotide 58

<400> 99

tacactgaat cttatataaa

20

<210> 100

<211> 36

<212> DNA

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oligonucleotide 59

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oligonucleotide 60

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oligonucleotide 61

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gggctttagg tttaccgttt tctgg 25

<210> 103  
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oligonucleotide 62

<400> 103  
ttctggacaa atattaagtt tttatcaa 28

<210> 104  
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oligonucleotide 63

<400> 104  
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 <400> 105  
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<210> 106  
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     oligonucleotide 65  
  
 <400> 106  
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<210> 107  
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 gaggaacttt taaatcaaca aataac 26

<210> 108  
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<210> 109  
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oligonucleotide 68

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tctttttaatt tatatcaacg ttc

23

<210> 110

<211> 21

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oligonucleotide 69

<400> 110

ccttcaaaat tttttggctg a

21

<210> 111

<211> 17

<212> DNA

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ttggctgaac gaaatga

17

<210> 112

<211> 23

<212> DNA

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oligonucleotide 71

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cgaaatgaaa cacgaaattt aag

23

<210> 113

<211> 37

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acacgaaatt taagtttatt acgtgctcaa tttatag 37

<210> 114  
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oligonucleotide 73

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gctcaattta tagctttaga acttgaattt ttaaattgcta ttccattg 48

<210> 115  
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oligonucleotide 74

<400> 115  
ccattgtttg cattaaatgg acagcag 27

<210> 116  
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oligonucleotide 75

<400> 116  
ccattgtttg cattaaatgg acagcag 27

<210> 117  
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oligonucleotide 76

<400> 117  
ccattactgt cattatatgc acaagct 27

<210> 118  
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oligonucleotide 77

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tatgcacaag ctttaaattt acatttg

27

<210> 119  
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oligonucleotide 78

<400> 119  
ttattaaaag aagcatctct ttt

23

<210> 120  
<211> 25  
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oligonucleotide 79

<400> 120  
tggagaagga tttggattca cacag

25

<210> 121  
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<220>  
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oligonucleotide 80

<400> 121  
cacatattat gaacgtcaat tgga

24

<210> 122  
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oligonucleotide 81

<400> 122  
tactgtgaaa ctttttataa tacagggt 28

<210> 123  
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<220>  
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oligonucleotide 82

<400> 123  
tacagggtta gaacgttta gagga 25

<210> 124  
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oligonucleotide 83

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aatactgaaa gttttttaag atatcatc 28

<210> 125  
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oligonucleotide 84

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gtagagaaat gactttatta ttattagaat tattagcgct atttccatat t 51

<210> 126  
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<220>  
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oligonucleotide 85

<400> 126  
atattatgaa ttacgacttt atccaac 27

<210> 127  
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<220>  
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oligonucleotide 86

<400> 127  
cttacacgtg agttatatac aga 23

<210> 128  
<211> 29  
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oligonucleotide 87

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tatacagaac cgattttatt taatccacc 29

<210> 129  
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oligonucleotide 88

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ccaccagcta atttaggact ttgccgac 28

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oligonucleotide 89

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<210> 131  
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oligonucleotide 90

<400> 131

catctttttg aaaggctgaa tag

23

<210> 132

<211> 30

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oligonucleotide 91

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taatcgattt ccattatcat ctaattttat

30

<210> 133

<211> 36

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oligonucleotide 92

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36

<210> 134

<211> 33

<212> DNA

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<223> Artificial sequence description:  
oligonucleotide 93

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tagttatctg aacgaatcag cattacaaga aga

33

<210> 135

<211> 20

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<223> Artificial sequence description:  
oligonucleotide 94

<400> 135  
caagaagaaa gttatggcct 20

<210> 136  
<211> 35  
<212> DNA  
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oligonucleotide 95

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<210> 137  
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oligonucleotide 96

<400> 137  
gagtcaacgg cattagaatt tcgttctgca 30

<210> 138  
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oligonucleotide 97

<400> 138  
ggtatatatg gcttaaatag agcttc 26

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oligonucleotide 98

<400> 139  
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 <400> 140  
 ctgctaattgg aggatgtaga gaactctatg a 31  
  
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     oligonucleotide 100  
  
 <400> 141  
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     oligonucleotide 101  
  
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 <210> 143  
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<400> 148  
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<400> 153

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29

<210> 156

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<400> 156

caagagattc taacattaaa tgcagaaggt

30

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<400> 157  
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<400> 158  
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<210> 160  
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